Figure 1: Nucleotide (SEQ ID NO: 1) and deduced amino acid sequence of human ChemR23 (AC075748)

1	M	E	D	E	D	Y	N	T	S	I	S	Y	G	D	E	15
175	ATG	GAG	GAT	GAA	GAT	TAC	AAC	ACT	TCC	ATC	AGT	TAC	GGT	GAT	GAA	219
16	Y	P	D	Y	L	D	S	I	V	V	L	E	D	L	S	30
220	TAC	CCT	GAT	TAT	TTA	GAC	TCC	ATT	GTG	GTT	TTG	GAG	GAC	TTA	TCC	264
31	P	L	E	A	R	V	T	R	I	F	L	V	V	V	Y	45
265	CCC	TTG	GAA	GCC	AGG	GTG	ACC	AGG	ATC	TTC	CTG	GTG	GTG	GTC	TAC	309
46	S	I	V	C	F	L	G	I	L	G	N	G	L	V	I	60
310	AGC	ATC	GTC	TGC	TTC	CTC	GGG	ATT	CTG	GGC	AAT	GGT	CTG	GTG	ATC	354
61	I	I	A	T	F	K	M	K	K	T	V	N	M	V	W	75
355	ATC	ATT	GCC	ACC	TTC	AAG	ATG	AAG	AAG	ACA	GTG	AAC	ATG	GTC	TGG	399
76	F	L	N	L	A	V	A	D	F	L	F	N	V	F	L	90
400	TTC	CTC	AAC	CTG	GCA	GTG	GCA	GAT	TTC	CTG	TTC	AAC	GTC	TTC	CTC	444
91	P	I	H	I	T	Y	A	A	M	D	Y	H	W	V	F	105
445	CCA	ATC	CAT	ATC	ACC	TAT	GCC	GCC	ATG	GAC	TAC	CAC	TGG	GTT	TTC	489
106	G	T	A	M	C	K	I	S	N	F	L	L	I	H	N	120
490	GGG	ACA	GCC	ATG	TGC	AAG	ATC	AGC	AAC	TTC	CTT	CTC	ATC	CAC	AAC	534
121	M	F	T	S	V	F	L	L	T	I	I	S	S	D	R	135
535	ATG	TTC	ACC	AGC	GTC	TTC	CTG	CTG	ACC	ATC	ATC	AGC	TCT	GAC	CGC	579
136	C	I	S	V	L	L	P	V	W	S	Q	N	H	R	S	150
580	TGC	ATC	TCT	GTG	CTC	CTC	CCT	GTC	TGG	TCC	CAG	AAC	CAC	CGC	AGC	624
151	V	R	L	A	Y	M	A	C	M	V	I	W	V	L	A	165
625	GTT	CGC	CTG	GCT	TAC	ATG	GCC	TGC	ATG	GTC	ATC	TGG	GTC	CTG	GCT	669
166	F	F	L	S	S	P	S	L	V	F	R	D	T	A	N	180
670	TTC	TTC	TTG	AGT	TCC	CCA	TCT	CTC	GTC	TTC	CGG	GAC	ACA	GCC	AAC	714
181	L	H	G	K	I	S	C	F	N	N	F	S	L	S	T	195
715	CTG	CAT	GGG	AAA	ATA	TCC	TGC	TTC	AAC	AAC	TTC	AGC	CTG	TCC	ACA	759
196	P	G	S	S	S	W	P	T	H	S	Q	M	D	P	V	210
760	CCT	GGG	TCT	TCC	TCG	TGG	CCC	ACT	CAC	TCC	CAA	ATG	GAC	CCT	GTG	804
211	G	Y	S	R	H	M	V	V	T	V	T	R	F	L	C	225
805	GGG	TAT	AGC	CGG	CAC	ATG	GTG	GTG	ACT	GTC	ACC	CGC	TTC	CTC	TGT	849
226	G	F	L	V	P	V	L	I	I	T	A	C	Y	L	T	240
850	GGC	TTC	CTG	GTC	CCA	GTC	CTC	ATC	ATC	ACA	GCT	TGC	TAC	CTC	ACC	894
241	I	V	C	K	L	Q	R	N	R	L	A	K	T	K	K	255
895	ATC	GTC	TGC	AAA	CTG	CAG	CGC	AAC	CGC	CTG	GCC	AAG	ACC	AAG	AAG	939
256	P	F	K	I	I	V	T	I	I	I	T	F	F	L	C	270
940	CCC	TTC	AAG	ATT	ATT	GTG	ACC	ATC	ATC	ATT	ACC	TTC	TTC	CTC	TGC	984

271	W	C	P	Y	H	T	L	N	L	L	E	L	H	H	T	285
985	TGG	TGC	CCC	TAC	CAC	ACA	CTC	AAC	CTC	CTA	GAG	CTC	CAC	CAC	ACT	1029
286	A	M	P	G	S	V	F	S	L	G	L	P	L	A	T	300
1030	GCC	ATG	CCT	GGC	TCT	GTC	TTC	AGC	CTG	GGT	TTG	CCC	CTG	GCC	ACT	1074
301	A	L	A	I	A	N	S	C	M	N	P	I	L	Y	V	315
1075	GCC	CTT	GCC	ATT	GCC	AAC	AGC	TGC	ATG	AAC	CCC	ATT	CTG	TAT	GTT	1119
316	F	M	G	Q	D	F	K	K	F	K	V	A	L	F	S	330
1120	TTC	ATG	GGT	CAG	GAC	TTC	AAG	AAG	TTC	AAG	GTG	GCC	CTC	TTC	TCT	1164
331	R	L	V	N	A	L	S	E	D	T	G	H	S	S	Y	345
1165	CGC	CTG	GTC	AAT	GCT	CTA	AGT	GAA	GAT	ACA	GGC	CAC	TCT	TCC	TAC	1209
346	P	S	H	R	S	F	T	K	M	S	S	M	N	E	R	360
1210	CCC	AGC	CAT	AGA	AGC	TTT	ACC	AAG	ATG	TCA	TCA	ATG	AAT	GAG	AGG	1254
361	T	S	M	N	E	R	E	T	G	M	L	*				372
1255	ACT	TCT	ATG	AAT	GAG	AGG	GAG	ACC	GGC	ATG	CTT	TGA				1290

Figure 2: Amino acid sequence of human ChemR23 (371 amino acids) (SEQ ID NO 2). The seven predicted transmembrane domaines are underlined. The consensus sequence for *N*-linked glycosylation (N-X-S/T) in the N terminus is bold and the potential site of phosphorylation by PKC (S/T-X-R/K) in the C terminus is in italic.

MEDEDY**NTS**ISYGDEYPDYLDSIVVLEDLSPLEARVTRIFLVVVYSIVCFLGILGNGLVIIIAT
FKMKKTVNMVWFLNLAVADFLFNVFLPIHITYAAMDYHWVFGTAMCKISNFLLIHNMFTSVFLL
TIISSDRCISVLLPVWSQNHRSVRLAYMACMVIWVLAFFLSSPSLVFRDTANLHGKISCFNNFS
LSTPGSSSWPTHSQMDPVGYSRHMVVTVTRFLCGFLVPVLIITACYLTIVCKLQRNRLAKTKKP
FKIIVTIIITFFLCWCPYHTLNLLELHHTAMPGSVFSLGLPLATALAIANSCMNPILYVFMGQD
FKKFKVALFSRLVNALSEDTGHSSYP*SHR*SFTKMSSMNERTSMNERETGML

Figure 3: Nucleotide and deduced amino acid sequence of mouse dez (AC u79525 – SEQ ID NOs:3 and 4, respectively)

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   1 M   E   Y   D   A   Y   N   D   S   G   I   Y   D   D   E      15
 265 ATG GAG TAC GAC GCT TAC AAC GAC TCC GGC ATC TAT GAT GAT GAG     309

  16 Y   S   D   G   F   G   Y   F   V   D   L   E   E   A   S      30
 310 TAC TCT GAT GGC TTT GGC TAC TTT GTG GAC TTG GAG GAG GCG AGT     354

  31 P   W   E   A   K   V   A   P   V   F   L   V   V   I   Y      45
 355 CCG TGG GAG GCC AAG GTG GCC CCG GTC TTC CTG GTG GTG ATC TAC     399

  46 S   L   V   C   F   L   G   L   L   G   N   G   L   V   I      60
 400 AGC TTG GTG TGC TTC CTC GGT CTC CTA GGC AAC GGC CTG GTG ATT     444

  61 V   I   A   T   F   K   M   K   K   T   V   N   T   V   W      75
 445 GTC ATC GCC ACC TTC AAG ATG AAG AAG ACC GTG AAC ACT GTG TGG     489

  76 F   V   N   L   A   V   A   D   F   L   F   N   I   F   L      90
 490 TTT GTC AAC CTG GCT GTG GCC GAC TTC CTG TTC AAC ATC TTT TTG     534

  91 P   M   H   I   T   Y   A   A   M   D   Y   H   W   V   F     105
 535 CCG ATG CAC ATC ACC TAC GCG GCC ATG GAC TAC CAC TGG GTG TTC     579

 106 G   K   A   M   C   K   I   S   N   F   L   L   S   H   N     120
 580 GGG AAG GCC ATG TGC AAG ATC AGC AAC TTC TTG CTC AGC CAC AAC     624

 121 M   Y   T   S   V   F   L   L   T   V   I   S   F   D   R     135
 625 ATG TAC ACC AGC GTC TTC CTG CTG ACT GTC ATC AGC TTT GAC CGC     669

 136 C   I   S   V   L   L   P   V   W   S   Q   N   H   R   S     150
 670 TGC ATC TCC GTG CTG CTC CCC GTC TGG TCC CAG AAC CAC CGC AGC     714

 151 I   R   L   A   Y   M   T   C   S   A   V   W   V   L   A     165
 715 ATC CGC CTG GCC TAC ATG ACC TGC TCG GCC GTC TGG GTC CTG GCT     759

 166 F   F   L   S   S   P   S   L   V   F   R   D   T   A   N     180
 760 TTC TTC TTG AGC TCC CCG TCC CTT GTC TTC CGG GAC ACC GCC AAC     804

 181 I   H   G   K   I   T   C   F   N   N   F   S   L   A   A     195
 805 ATT CAT GGG AAG ATA ACC TGC TTC AAC AAC TTC AGC TTG GCC GCG     849

 196 P   E   S   S   P   H   P   A   H   S   Q   V   V   S   T     210
 850 CCT GAG TCC TCC CCA CAT CCC GCC CAC TCG CAA GTA GTT TCC ACA     894

 211 G   Y   S   R   H   V   A   V   T   V   T   R   F   L   C     225
 895 GGG TAC AGC AGA CAC GTG GCG GTC ACT GTC ACC CGC TTC CTT TGC     939

 226 G   F   L   I   P   V   F   I   I   T   A   C   Y   L   T     240
 940 GGC TTC CTG ATC CCC GTC TTC ATC ATC ACG GCC TGC TAC CTT ACC     984

 241 I   V   F   K   L   Q   R   N   R   L   A   K   N   K   K     255
 985 ATC GTC TTC AAG CTG CAG CGC AAC CGC CTG GCC AAG AAC AAG AAG    1029

 256 P   F   K   I   I   I   T   I   I   I   T   F   F   L   C     270
1030 CCC TTC AAG ATC ATC ATC ACC ATC ATC ATC ACC TTC TTC CTC TGC    1074

 271 W   C   P   Y   H   T   L   Y   L   L   E   L   H   H   T     285
1075 TGG TGC CCC TAC CAC ACC CTC TAC CTG CTG GAG CTC CAC CAC ACA    1119

 286 A   V   P   S   S   V   F   S   L   G   L   P   L   A   T     300
1120 GCT GTG CCA AGC TCT GTC TTC AGC CTG GGG CTA CCC CTG GCC ACG    1164
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301	A	V	A	I	A	N	S	C	M	N	P	I	L	Y	V	315
1165	GCC	GTC	GCC	ATC	GCC	AAC	AGC	TGC	ATG	AAC	CCC	ATT	CTG	TAC	GTC	1209
316	F	M	G	H	D	F	R	K	F	K	V	A	L	F	S	330
1210	TTC	ATG	GGC	CAC	GAC	TTC	AGA	AAA	TTC	AAG	GTG	GCC	CTC	TTC	TCC	1254
331	R	L	A	N	A	L	S	E	D	T	G	P	S	S	Y	345
1255	CGC	CTG	GCC	AAC	GCC	CTG	AGT	GAG	GAC	ACA	GGC	CCC	TCC	TCC	TAC	1299
346	P	S	H	R	S	F	T	K	M	S	S	L	N	E	K	360
1300	CCC	AGT	CAC	AGG	AGC	TTC	ACC	AAG	ATG	TCG	TCT	TTG	AAT	GAG	AAG	1344
361	A	S	V	N	E	K	E	T	S	T	L	*				372
1345	GCT	TCG	GTG	AAT	GAG	AAG	GAG	ACC	AGT	ACC	CTC	TGA				1380

Figure 4: Nucleotide and deduced amino acid sequence of rat G-protein coupled chemoattractant-1 (AC NM_022218 - SEQ ID Nos: 5 and 6, respectively).

1 M E Y E G Y N D S S I Y G E E 15
1 ATG GAG TAC GAG GGT TAC AAC GAC TCC AGC ATC TAC GGT GAG GAG 45

16 Y S D G S D Y I V D L E E A G 30
46 TAT TCT GAC GGC TCG GAC TAC ATC GTG GAC TTG GAG GAG GCG GGT 90

31 P L E A K V A E V F L V V I Y 45
91 CCA CTG GAG GCC AAG GTG GCC GAG GTC TTC CTG GTG GTA ATC TAC 135

46 S L V C F L G I L G N G L V I 60
136 AGC TTG GTG TGC TTC CTC GGG ATC CTA GGC AAT GGC CTG GTG ATT 180

61 V I A T F K M K K T V N T V W 75
181 GTC ATC GCC ACC TTC AAG ATG AAG AAG ACG GTG AAC ACC GTG TGG 225

76 F V N L A V A D F L F N I F L 90
226 TTT GTC AAC CTG GCC GTG GCT GAC TTC CTG TTC AAC ATC TTC TTG 270

91 P I H I T Y A A M D Y H W V F 105
271 CCC ATC CAC ATC ACC TAT GCC GCT ATG GAC TAC CAC TGG GTG TTC 315

106 G K A M C K I S S F L L S H N 120
316 GGG AAA GCC ATG TGC AAG ATT AGT AGC TTT CTG CTA AGC CAC AAC 360

121 M Y T S V F L L T V I S F D R 135
361 ATG TAC ACC AGC GTC TTC CTG CTC ACT GTC ATC AGC TTC GAC CGC 405

136 C I S V L L P V W S Q N H R S 150
406 TGC ATC TCC GTG CTC CTC CCC GTC TGG TCC CAG AAC CAC CGC AGC 450

151 V R L A Y M T C V V V W V W L 165
451 GTG CGT CTG GCC TAC ATG ACC TGC GTG GTT GTC TGG GTC TGG CTT 495

166 S S E S P P S L V F G H V S T 180
496 TCT TCT GAG TCT CCC CCG TCC CTC GTC TTC GGA CAC GTC AGC ACC 540

181 S H G K I T C F N N F S L A A 195
541 AGC CAC GGG AAG ATA ACC TGC TTC AAC AAC TTC AGC CTG GCG GCG 585

196 P E P F S H S T H P R T D P V 210
586 CCC GAG CCT TTC TCT CAT TCC ACC CAC CCG CGA ACA GAC CCG GTA 630

211 G Y S R H V A V T V T R F L C 225
631 GGG TAC AGC AGA CAT GTG GCG GTC ACC GTC ACC CGC TTC CTC TGT 675

226 G F L I P V F I I T A C Y L T 240
676 GGC TTC CTG ATC CCC GTC TTC ATC ATC ACG GCC TGT TAC CTC ACC 720

241 I V F K L Q R N R Q A K T K K 255
721 ATC GTC TTC AAG TTG CAG CGC AAC CGC CAG GCC AAG ACC AAG AAG 765

256 P F K I I I T I I I T F F L C 270
766 CCC TTC AAG ATC ATC ATC ACC ATC ATC ATC ACC TTC TTC CTC TGC 810

271 W C P Y H T L Y L L E L H H T 285
811 TGG TGC CCC TAC CAC ACA CTC TAC CTG CTG GAG CTC CAC CAC ACG 855

286 A V P A S V F S L G L P L A T 300

856 GCT GTG CCA GCC TCT GTC TTC AGC CTG GGA CTG CCC CTG GCC ACA 900

301 A V A I A N S C M N P I L Y V 315
901 GCC GTC GCC ATC GCC AAC AGC TGT ATG AAC CCC ATC CTG TAC GTC 945

316 F M G H D F K K F K V A L F S 330
946 TTC ATG GGC CAC GAC TTC AAA AAA TTC AAG GTG GCC CTT TTC TCC 990

331 R L V N A L S E D T G P S S Y 345
991 CGC CTG GTG AAT GCC CTG AGC GAG GAC ACA GGA CCC TCC TCC TAC 1035

346 P S H R S F T K M S S L I E K 360
1036 CCC AGT CAC AGG AGC TTC ACC AAG ATG TCC TCA TTG ATT GAG AAG 1080

361 A S V N E K E T S T L * 372
1081 GCT TCA GTG AAT GAG AAA GAG ACC AGC ACC CTC TGA 1116

Figure 5: Alignment of ChemR23

Alignment of the amino acid sequence of ChemR23 with AT2 receptors, C3a, C5a and fMLP receptor and other chemoattractants related sequences were performed using ClustalX algorithm. Then, the dendrogram was constucted using TreeView algorithm.

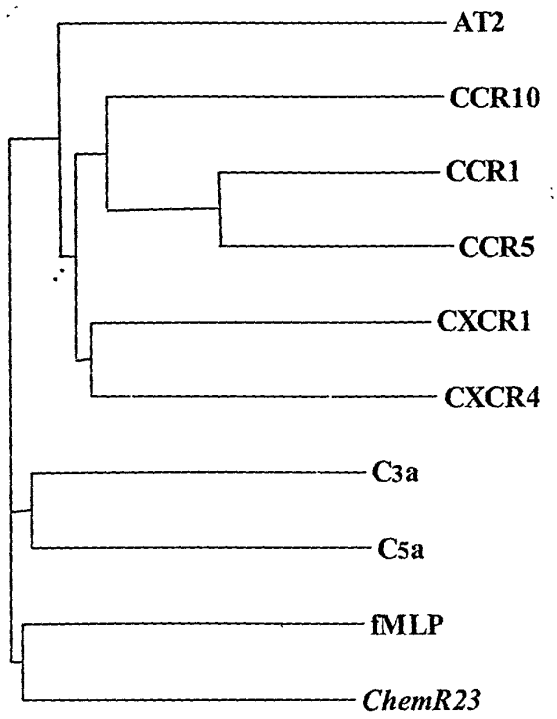

Figure 6: Nucleotide and deduced amino acid sequence of human Tig2 (AC Q99969 - SEQ ID Nos: 7 and 8, respectively)

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  1  M   R   R   L   L   I   P   L   A   L   W   L   G   A   V     15
 97 ATG CGA CGG CTG CTG ATC CCT CTG GCC CTG TGG CTG GGT GCG GTG    141

 16  G   V   G   V   A   E   L   T   E   A   Q   R   R   G   L     30
142 GGC GTG GGC GTC GCC GAG CTC ACG GAA GCC CAG CGC CGG GGC CTG    186

 31  Q   V   A   L   E   E   F   H   K   H   P   P   V   Q   W     45
187 CAG GTG GCC CTG GAG GAA TTT CAC AAG CAC CCG CCC GTG CAG TGG    231

 46  A   F   Q   E   T   S   V   E   S   A   V   D   T   P   F     60
232 GCC TTC CAG GAG ACC AGT GTG GAG AGC GCC GTG GAC ACG CCC TTC    276

 61  P   A   G   I   F   V   R   L   E   F   K   L   Q   Q   T     75
277 CCA GCT GGA ATA TTT GTG AGG CTG GAA TTT AAG CTG CAG CAG ACA    321

 76  S   C   R   K   R   D   W   K   K   P   E   C   K   V   R     90
322 AGC TGC CGG AAG AGG GAC TGG AAG AAA CCC GAG TGC AAA GTC AGG    366

 91  P   N   G   R   K   R   K   C   L   A   C   I   K   L   G    105
367 CCC AAT GGG AGG AAA CGG AAA TGC CTG GCC TGC ATC AAA CTG GGC    411

106  S   E   D   K   V   L   G   R   L   V   H   C   P   I   E    120
412 TCT GAG GAC AAA GTT CTG GGC CGG TTG GTC CAC TGC CCC ATA GAG    456

121  T   Q   V   L   R   E   A   E   E   H   Q   E   T   Q   C    135
457 ACC CAA GTT CTG CGG GAG GCT GAG GAG CAC CAG GAG ACC CAG TGC    501

136  L   R   V   Q   R   A   G   E   D   P   H   S   F   Y   F    150
502 CTC AGG GTG CAG CGG GCT GGT GAG GAC CCC CAC AGC TTC TAC TTC    546

151  P   G   Q   F   A   F   S   K   A   L   P   R   S   *        164
547 CCT GGA CAG TTC GCC TTC TCC AAG GCC CTG CCC CGC AGC TAA        588
```

Figure 7: Nucleotide and deduced amino acid sequence of mouse Tig2 (SEQ ID Nos: 9 and 10, respectively)

```
  1  M   K   C   L   L   I   S   L   A   L   W   L   G   T   V     15
102 ATG AAG TGC TTG CTG ATC TCC CTA GCC CTA TGG CTG GGC ACA GTG    146

 16  G   T   R   G   T   E   P   E   L   S   E   T   Q   R   R     30
147 GGC ACA CGT GGG ACA GAG CCC GAA CTC AGC GAG ACC CAG CGC AGG    191

 31  S   L   Q   V   A   L   E   E   F   H   K   H   P   P   V     45
192 AGC CTA CAG GTG GCT CTG GAG GAG TTC CAC AAA CAC CCA CCT GTG    236

 46  Q   L   A   F   Q   E   I   G   V   D   R   A   E   E   V     60
237 CAG TTG GCC TTC CAA GAG ATC GGT GTG GAC AGA GCT GAA GAA GTG    281

 61  L   F   S   A   G   T   F   V   R   L   E   F   K   L   Q     75
282 CTC TTC TCA GCT GGC ACC TTT GTG AGG TTG GAA TTT AAG CTC CAG    326

 76  Q   T   N   C   P   K   K   D   W   K   K   P   E   C   T     90
327 CAG ACC AAC TGC CCC AAG AAG GAC TGG AAA AAG CCG GAG TGC ACA    371

 91  I   K   P   N   G   R   R   R   K   C   L   A   C   I   K    105
372 ATC AAA CCA AAC GGG AGA AGG CGG AAA TGC CTG GCC TGC ATT AAA    416

106  M   D   P   K   G   K   I   L   G   R   I   V   H   C   P    120
417 ATG GAC CCC AAG GGT AAA ATT CTA GGC CGG ATA GTC CAC TGC CCA    461

121  I   L   K   Q   G   P   Q   D   P   Q   E   L   Q   C   I    135
462 ATT CTG AAG CAA GGG CCT CAG GAT CCT CAG GAG TTG CAA TGC ATT    506

136  K   I   A   Q   A   G   E   D   P   H   G   Y   F   L   P    150
507 AAG ATA GCA CAG GCT GGC GAA GAC CCC CAC GGC TAC TTC CTA CCT    551

151  G   Q   F   A   F   S   R   A   L   R   T   K   *            163
552 GGA CAG TTT GCC TTC TCC AGG GCC CTG AGA ACC AAA TAA            590
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Figure 8: Amino acid sequence alignment of human and mouse TIG2. Identical and similar residues are shaded.

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        151              168
   mus  HGYFLPGQFA FSRALRTK
   rat  RIYFFPGQFA FSRAL~~~
  tig2  HSFYFPGQFA FSKALPRS
   sus  HSYYFPGQFA FFKALPPS
   bos  HSYYLPGQFA FIKAL~~~
gallus  DVLYLPGMFA FSKGLP~~
```

Identities :

	bos.pep	mus.pep	sus.pep	gallus	rat.pep
tig2.pep	83.750	56.250	86.503	30.675	61.392
bos.pep		54.375	87.500	31.875	56.329
mus.pep			54.375	31.677	73.125
sus.pep				31.288	58.228
gallus.pep					30.818

Figure 11: Primary screening of HPLC fractions obtained from the fractionation of human ovary ascites.

The different fractions obtained following fractionation of human ovary ascites were diluted fivefold in the buffer assay and tested in aequorin assay using a cell line expressing ChemR23 (open circles) or cell lines expressing not related receptors (closed triangles and squares). The response obtained for each fraction was normalized using the ATP response of each cell line.

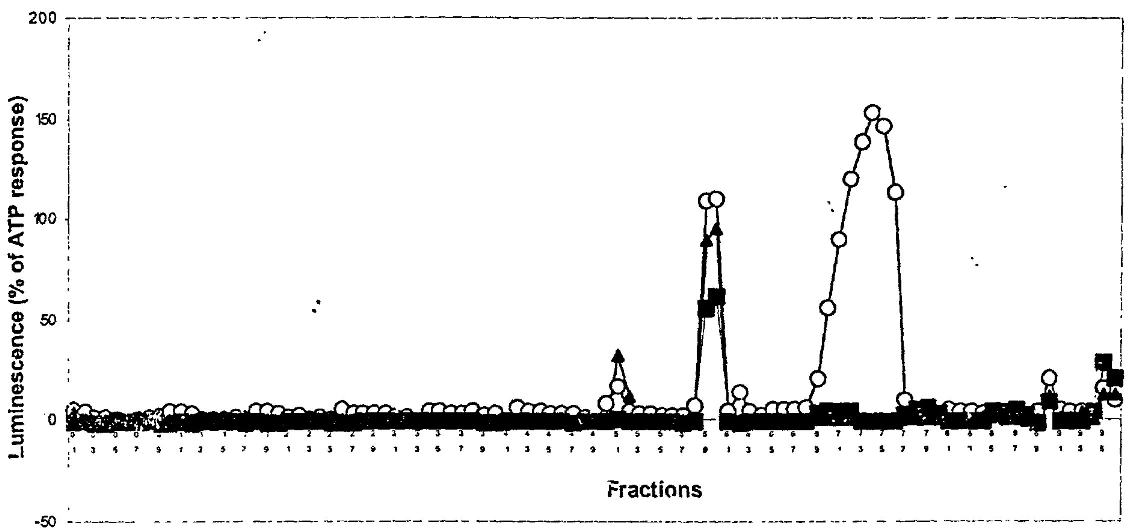

Figure 12: Activation of ChemR23 by cells transfected with TIG2

293 T cells were transiently transfected with pCDNA3- TIG2 or with pCDNA3 alone (mock transfected). Increasing volumes of the supernatant collected 4 days following transfection were analysed in a aequorin-based assay with CHO cells expressing ChemR23. A representative experiment is shown. Assay was performed in triplicate and SD are indicated.

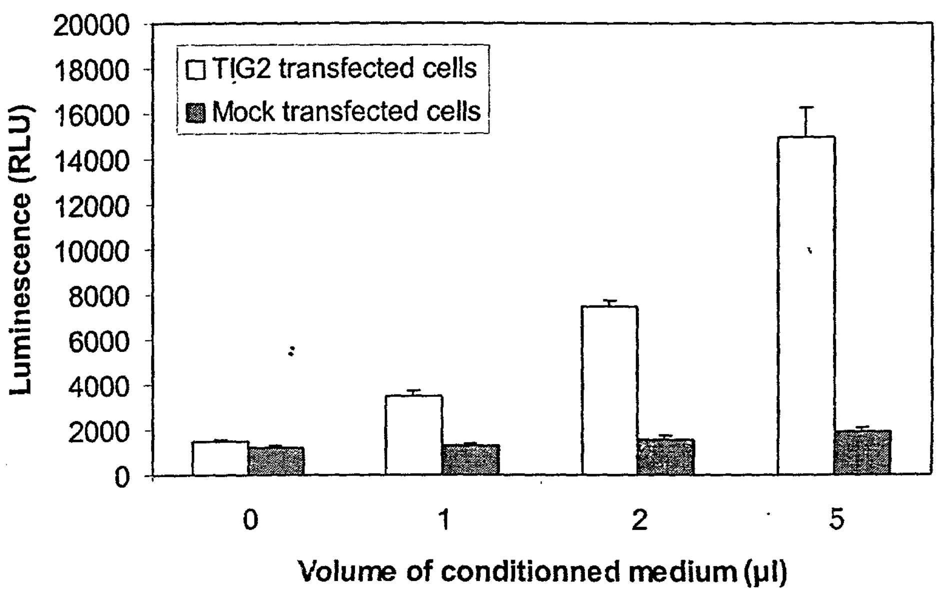

Figure 13: Characterization of antibodies directed against ChemR23
A mixture of recombinant cells made up of 2/3 recombinant ChemR23 CHO cells and 1/3 recombinant HCR CHO cells (negative control) was subject to react with either a supernatant of the anti ChemR23 5C 1H2 monoclonal antibody (thick line) or a supernatant with no known antibody activity (thin line, grey filling). After staining with FITC labeled anti mouse Ig these preparations were analysed by flow cytofluorometry. Results are displayed as a histogram of the number of cells (Events axis) expressing a given fluorescence (FL1-H axis). Monoclonal 5C 1H2 allowed to discriminate the ChemR23 recombinant sub-population of cells from the negative control cells as evidenced by the relative proportions of both type of cells. The background fluorescence of the assay is given by the second staining (grey filling).